



## SEQUENCE LISTING

<110> Shaaltiel, Yoseph  
<120> CELL/TISSUE CULTURING DEVICE, SYSTEM AND METHOD  
<130> 27557  
<160> 14  
<170> PatentIn version 3.2  
<210> 1  
<211> 22  
<212> PRT  
<213> Artificial sequence  
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<223> Signal Peptide for the ER  
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Met Lys Thr Asn Leu Phe Leu Phe Leu Ile Phe Ser Leu Leu Leu Ser  
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Leu Ser Ser Ala Glu Phe  
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<223> Vacuolar targeting signal from Tobacco chitinase A  
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Asp Leu Leu Val Asp Thr Met  
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<223> Single strand DNA oligonucleotide  
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cagaattcgc ccgccctgc a 21  
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<223> Single strand DNA oligonucleotide  
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ctcagatctt ggcgatgccca ca 22  
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<212> DNA  
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<220>  
 <223> Single strand DNA oligonucleotide  
  
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 <223> Single strand DNA oligonucleotide  
  
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 <211> 1491  
 <212> DNA  
 <213> Homo sapiens  
  
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 gagagtacac gcagtggcg acggatggag ctgagtatgg ggcccatcca ggctaatac 180  
 acgggcacag gcctgctact gaccctgcag ccagaacaga agttccagaa agtgaaggga 240  
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 caaaatttgc tacttaaatc gtacttctct gaagaaggaa tcggatataa catcatccgg 360  
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 cccggagaca tctaccacca gacctgggc agatactttg tgaagttcct ggatgcctat 660  
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1491

<210> 8  
 <211> 497  
 <212> PRT  
 <213> Homo sapiens

<400> 8

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 20 25 30

Ala Leu Gly Thr Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg Arg  
 35 40 45

Met Glu Leu Ser Met Gly Pro Ile Gln Ala Asn His Thr Gly Thr Gly  
 50 55 60

Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys Phe Gln Lys Val Lys Gly  
 65 70 75 80

Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu Asn Ile Leu Ala Leu  
 85 90 95

Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe Ser Glu Glu  
 100 105 110

Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp Phe  
 115 120 125

Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp Phe Gln Leu  
 130 135 140

His Asn Phe Ser Leu Pro Glu Glu Asp Thr Lys Leu Lys Ile Pro Leu  
 145 150 155 160

Ile His Arg Ala Leu Gln Leu Ala Gln Arg Pro Val Ser Leu Leu Ala  
 165 170 175

Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys Thr Asn Gly Ala Val Asn  
 180 185 190

Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile Tyr His Gln Thr  
 195 200 205

Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala Glu His Lys  
 210 215 220

Leu Gln Phe Trp Ala Val Thr Ala Glu Asn Glu Pro Ser Ala Gly Leu  
 225 230 235 240

Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro Glu His Gln  
 245 250 255

Arg Asp Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala Asn Ser Thr  
 260 265 270  
 His His Asn Val Arg Leu Leu Met Leu Asp Asp Gln Arg Leu Leu Leu  
 275 280 285  
 Pro His Trp Ala Lys Val Val Leu Thr Asp Pro Glu Ala Ala Lys Tyr  
 290 295 300  
 Val His Gly Ile Ala Val His Trp Tyr Leu Asp Phe Leu Ala Pro Ala  
 305 310 315 320  
 Lys Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro Asn Thr Met Leu  
 325 330 335  
 Phe Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser Val  
 340 345 350  
 Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile  
 355 360 365  
 Thr Asn Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala  
 370 375 380  
 Leu Asn Pro Glu Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser  
 385 390 395 400  
 Pro Ile Ile Val Asp Ile Thr Lys Asp Thr Phe Tyr Lys Gln Pro Met  
 405 410 415  
 Phe Tyr His Leu Gly His Phe Ser Lys Phe Ile Pro Glu Gly Ser Gln  
 420 425 430  
 Arg Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu Asp Ala Val Ala  
 435 440 445  
 Leu Met His Pro Asp Gly Ser Ala Val Val Val Val Leu Asn Arg Ser  
 450 455 460  
 Ser Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu  
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 Glu Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp His Arg  
 485 490 495

Gln

<210> 9  
 <211> 338  
 <212> DNA  
 <213> Artificial sequence  
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 <223> CaMV 35S Promoter nucleic acid sequence

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 ttcatcgaaa ggacagtaga aaaggaaggt ggctcctaca aatgccatca ttgcgataaa 120  
 ggaaaggcta tcgttcaaga tgccctctacc gacagtggtc ccaaagatgg acccccaccc 180  
 acgaggaaca tcgtggaaaa agaagacgtt ccaaccacgt cttcaaagca agtggattga 240  
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<210> 10  
 <211> 66  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Nucleic acid sequence encoding the ER signal peptide

<400> 10  
 atgaagacta atctttttct ctttctcctc ttttcacttc tctatcatt atcctcgcc 60  
 gaattc 66

<210> 11  
 <211> 21  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Nucleic acid sequence encoding the vacuolar targeting sequence

<400> 11  
 gatcttttag tcgatactat g 21

<210> 12  
 <211> 167  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Sequence for terminator

<220>  
 <221> misc\_feature  
 <222> (162)..(162)  
 <223> n is a, c, g, or t

<400> 12  
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 tttataataa acaaagactt tgtcccaaaa accccccccc cngcaga 167

<210> 13  
 <211> 2186  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Nucleic acid encoding recombinant GCD fused to signal peptides

<220>  
 <221> misc\_feature

<222> (2181)..(2181)

<223> n is a, c, g, or t

<400> 13

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ggaaaggcta tcgttcaaga tgcctctacc gacagtgggc ccaaagatgg acccccaccc	180
acgaggaaca tcgtggaaaa agaagacgtt ccaaccacgt cttcaaagca agtggattga	240
tgtgatattc ccactgacgt aagggatgac gcacaatccc actatccttc gcaagacctt	300
tcctctatat aaggaagttc atttcatttg gagaggacag gcttcttgag atccttcaac	360
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tgtattccct tgcaatgcag ggcctagggc tatgaataaa gttaatgtgt gaatgtgtga	2100

atgtgtgatt gtgacctgaa gggatcacga ctataatcgt ttataataaa caaagacttt 2160

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<210> 14

<211> 526

<212> PRT

<213> Artificial sequence

<220>

<223> Recombinant GCD fused to signal peptides

<400> 14

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Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser Phe  
35 40 45

Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu Ser  
50 55 60

Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln Ala  
65 70 75 80

Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys  
85 90 95

Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala Ala  
100 105 110

Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys  
115 120 125

Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro  
130 135 140

Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr  
145 150 155 160

Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp Thr  
165 170 175

Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln Arg  
180 185 190

Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys  
195 200 205

Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly  
210 215 220

Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp

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Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu Asn						
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Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly						
	260			265		270
Phe Thr Pro Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly Pro						
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Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu Asp						
	290			295		300
Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr Asp						
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Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr Leu						
	325			330		335
Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg Leu						
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Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser Lys						
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Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met Gln						
	370			375		380
Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly Trp						
	385			390		395
Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp Val						
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Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr Lys Asp Thr						
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Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys Phe						
	435			440		445
Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys Asn						
	450			455		460
Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val Val						
	465			470		475
Val Val Leu Asn Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys Asp						
	485			490		495
Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile His						
	500			505		510
Thr Tyr Leu Trp His Arg Gln Asp Leu Leu Val Asp Thr Met						
	515			520		525